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TECH CENTER 1600/2900



1652

RAW SEQUENCE LISTING

DATE: 01/24/2002

PATENT APPLICATION: US/09/902,651

TIME: 11:51:05

Input Set : A:\77670-593 Sequence Listing.txt

Output Set: N:\CRF3\01242002\I902651.raw

ENTERED

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4 <110> APPLICANT: NAKANE et al.
6 <120> TITLE OF INVENTION: FARNESYL DIPHOSPHATE SYNTHASE
8 <130> FILE REFERENCE: 77670-593
10 <140> CURRENT APPLICATION NUMBER: 09/902,651
11 <141> CURRENT FILING DATE: 2001-07-12
13 <150> PRIOR APPLICATION NUMBER: 08/898,560
14 <151> PRIOR FILING DATE: 1997-07-22
16 <150> PRIOR APPLICATION NUMBER: JP8-213211
17 <151> PRIOR FILING DATE: 1996-07-24
19 <160> NUMBER OF SEQ ID NOS: 14
21 <170> SOFTWARE: FastSEQ for Windows Version 4.0
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 330
25 <212> TYPE: PRT
26 <213> ORGANISM: Sulfolobus acidocaldarius
28 <400> SEQUENCE: 1
29 Met Ser Tyr Phe Asp Asn Tyr Phe Asn Glu Ile Val Asn Ser Val Asn
30 1 5 10 15
31 Asp Ile Ile Lys Ser Tyr Ile Ser Gly Asp Val Pro Lys Leu Tyr Glu
32 20 25 30
33 Ala Ser Tyr His Leu Phe Thr Ser Gly Gly Lys Arg Leu Arg Pro Leu
34 35 40 45
35 Ile Leu Thr Ile Ser Ser Asp Leu Phe Gly Gly Gln Arg Glu Arg Ala
36 50 55 60
37 Tyr Tyr Ala Gly Ala Ala Ile Glu Val Leu His Thr Phe Thr Leu Val
38 65 70 75 80
39 His Asp Asp Ile Met Asp Gln Asp Asn Ile Arg Arg Gly Leu Pro Thr
40 85 90 95
41 Val His Val Lys Tyr Gly Leu Pro Leu Ala Ile Leu Ala Gly Asp Leu
42 100 105 110
43 Leu His Ala Lys Ala Phe Gln Leu Leu Thr Gln Ala Leu Arg Gly Leu
44 115 120 125
45 Pro Ser Glu Thr Ile Ile Lys Ala Phe Asp Ile Phe Thr Arg Ser Ile
46 130 135 140
47 Ile Ile Ile Ser Glu Gly Gln Ala Val Asp Met Glu Phe Glu Asp Arg
48 145 150 155 160
49 Ile Asp Ile Lys Glu Gln Glu Tyr Leu Asp Met Ile Ser Arg Lys Thr
50 165 170 175
51 Ala Ala Leu Phe Ser Ala Ser Ser Ser Ile Gly Ala Leu Ile Ala Gly
52 180 185 190
53 Ala Asn Asp Asn Asp Val Arg Leu Met Ser Asp Phe Gly Thr Asn Leu
54 195 200 205
55 Gly Ile Ala Phe Gln Ile Val Asp Asp Ile Leu Gly Leu Thr Ala Asp

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56      210      215      220
57 Glu Lys Glu Leu Gly Lys Pro Val Phe Ser Asp Ile Arg Glu Gly Lys
58 225      230      235      240
59 Lys Thr Ile Leu Val Ile Lys Thr Leu Glu Leu Cys Lys Glu Asp Glu
60      245      250      255
61 Lys Lys Ile Val Leu Lys Ala Leu Gly Asn Lys Ser Ala Ser Lys Glu
62      260      265      270
63 Glu Leu Met Ser Ser Ala Asp Ile Ile Lys Lys Tyr Ser Leu Asp Tyr
64      275      280      285
65 Ala Tyr Asn Leu Ala Glu Lys Tyr Tyr Lys Asn Ala Ile Asp Ser Leu
66      290      295      300
67 Asn Gln Val Ser Ser Lys Ser Asp Ile Pro Gly Lys Ala Leu Lys Tyr
68 305      310      315      320
69 Leu Ala Glu Phe Thr Ile Arg Arg Arg Lys
70      325      330
73 <210> SEQ ID NO: 2
74 <211> LENGTH: 993
75 <212> TYPE: DNA
76 <213> ORGANISM: Sulfolobus acidocaldarius
78 <220> FEATURE:
79 <221> NAME/KEY: CDS
80 <222> LOCATION: (1)...(993)
82 <400> SEQUENCE: 2
83 atg agt tac ttt gac aac tat ttt aat gag att gtt aat tct gta aac 48
84 Met Ser Tyr Phe Asp Asn Tyr Phe Asn Glu Ile Val Asn Ser Val Asn
85 1 5 10 15
87 gac att att aag agc tat ata tct gga gat gtt cct aaa cta tat gaa 96
88 Asp Ile Ile Lys Ser Tyr Ile Ser Gly Asp Val Pro Lys Leu Tyr Glu
89 20 25 30
91 gcc tca tat cat ttg ttt aca tct gga ggt aag agg tta aga cca tta 144
92 Ala Ser Tyr His Leu Phe Thr Ser Gly Gly Lys Arg Leu Arg Pro Leu
93 35 40 45
95 atc tta act ata tca tca gat tta ttc gga gga cag aga gaa aga gct 192
96 Ile Leu Thr Ile Ser Ser Asp Leu Phe Gly Gly Gln Arg Glu Arg Ala
97 50 55 60
99 tat tat gca ggt gca gct att gaa gtt ctt cat act ttt acg ctt gtg 240
100 Tyr Tyr Ala Gly Ala Ala Ile Glu Val Leu His Thr Phe Thr Leu Val
101 65 70 75 80
103 cat gat gat att atg gat caa gat aat atc aga aga ggg tta ccc aca 288
104 His Asp Asp Ile Met Asp Gln Asp Asn Ile Arg Arg Gly Leu Pro Thr
105 85 90 95
107 gtc cac gtg aaa tac ggc tta ccc tta gca ata tta gct ggg gat tta 336
108 Val His Val Lys Tyr Gly Leu Pro Leu Ala Ile Leu Ala Gly Asp Leu
109 100 105 110
111 cta cat gca aag gct ttt cag ctc tta acc cag gct ctt aga ggt ttg 384
112 Leu His Ala Lys Ala Phe Gln Leu Leu Thr Gln Ala Leu Arg Gly Leu
113 115 120 125
115 cca agt gaa acc ata att aag gct ttc gat att ttc act cgt tca ata 432
116 Pro Ser Glu Thr Ile Ile Lys Ala Phe Asp Ile Phe Thr Arg Ser Ile
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117      130      135      140
119 ata att ata tcc gaa gga cag gca gta gat atg gaa ttt gag gac aga 480
120 Ile Ile Ile Ser Glu Gly Gln Ala Val Asp Met Glu Phe Glu Asp Arg
121 145      150      155      160
123 att gat ata aag gag cag gaa tac ctt gac atg atc tca cgt aag aca 528
124 Ile Asp Ile Lys Glu Gln Glu Tyr Leu Asp Met Ile Ser Arg Lys Thr
125      165      170      175
127 gct gca tta ttc tcg gca tcc tca agt ata ggc gca ctt att gct ggt 576
128 Ala Ala Leu Phe Ser Ala Ser Ser Ser Ile Gly Ala Leu Ile Ala Gly
129      180      185      190
131 gct aat gat aat gat gta aga ctg atg tct gat ttc ggt acg aat cta 624
132 Ala Asn Asp Asn Asp Val Arg Leu Met Ser Asp Phe Gly Thr Asn Leu
133      195      200      205
135 ggt att gca ttt cag att gtt gac gat atc tta ggt cta aca gca gac 672
136 Gly Ile Ala Phe Gln Ile Val Asp Asp Ile Leu Gly Leu Thr Ala Asp
137      210      215      220
139 gaa aag gaa ctt gga aag cct gtt ttt agt gat att agg gag ggt aaa 720
140 Glu Lys Glu Leu Gly Lys Pro Val Phe Ser Asp Ile Arg Glu Gly Lys
141 225      230      235      240
143 aag act ata ctt gta ata aaa aca ctg gag ctt tgt aaa gag gac gag 768
144 Lys Thr Ile Leu Val Ile Lys Thr Leu Glu Leu Cys Lys Glu Asp Glu
145      245      250      255
147 aag aag att gtc cta aag gcg tta ggt aat aag tca gcc tca aaa gaa 816
148 Lys Lys Ile Val Leu Lys Ala Leu Gly Asn Lys Ser Ala Ser Lys Glu
149      260      265      270
151 gaa tta atg agc tca gca gat ata att aag aaa tac tct tta gat tat 864
152 Glu Leu Met Ser Ser Ala Asp Ile Ile Lys Lys Tyr Ser Leu Asp Tyr
153      275      280      285
155 gca tac aat tta gca gag aaa tat tat aaa aat gct ata gac tct tta 912
156 Ala Tyr Asn Leu Ala Glu Lys Tyr Tyr Lys Asn Ala Ile Asp Ser Leu
157      290      295      300
159 aat caa gtc tcc tct aag agt gat ata cct gga aag gct tta aaa tat 960
160 Asn Gln Val Ser Ser Lys Ser Asp Ile Pro Gly Lys Ala Leu Lys Tyr
161 305      310      315      320
163 cta gct gaa ttt acg ata aga agg aga aaa taa 993
164 Leu Ala Glu Phe Thr Ile Arg Arg Arg Lys *
165      325      330
168 <210> SEQ ID NO: 3
169 <211> LENGTH: 37
170 <212> TYPE: DNA
171 <213> ORGANISM: Sulfolobus acidocaldarius
173 <400> SEQUENCE: 3
174 catacttttt tccttgtggc tgatgatatc atggatc 37
176 <210> SEQ ID NO: 4
177 <211> LENGTH: 37
178 <212> TYPE: DNA
179 <213> ORGANISM: Sulfolobus acidocaldarius
181 <400> SEQUENCE: 4
182 catacttttt tccttgtgct tgatgatatc atggatc 37
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184 <210> SEQ ID NO: 5
185 <211> LENGTH: 37
186 <212> TYPE: DNA
187 <213> ORGANISM: Sulfolobus acidocaldarius
189 <400> SEQUENCE: 5
190 cataacttatt tccttgtgct tgatgatatc atggatc 37
192 <210> SEQ ID NO: 6
193 <211> LENGTH: 37
194 <212> TYPE: DNA
195 <213> ORGANISM: Sulfolobus acidocaldarius
197 <400> SEQUENCE: 6
198 cataacttatt tccttgtggc tgatgatatc atggatc 37
200 <210> SEQ ID NO: 7
201 <211> LENGTH: 36
202 <212> TYPE: DNA
203 <213> ORGANISM: Sulfolobus acidocaldarius
205 <400> SEQUENCE: 7
206 gttcttcata cttattcgct tattcatgat agtatt 36
208 <210> SEQ ID NO: 8
209 <211> LENGTH: 33
210 <212> TYPE: DNA
211 <213> ORGANISM: Sulfolobus acidocaldarius
213 <400> SEQUENCE: 8
214 attcatgatg atcttccatc gatggatcaa gat 33
216 <210> SEQ ID NO: 9
217 <211> LENGTH: 27
218 <212> TYPE: DNA
219 <213> ORGANISM: Sulfolobus acidocaldarius
221 <400> SEQUENCE: 9
222 tttttccttg tggctgatga tatcatg 27
224 <210> SEQ ID NO: 10
225 <211> LENGTH: 27
226 <212> TYPE: DNA
227 <213> ORGANISM: Sulfolobus acidocaldarius
229 <400> SEQUENCE: 10
230 tttttccttg tgcttgatga tatcatg 27
232 <210> SEQ ID NO: 11
233 <211> LENGTH: 27
234 <212> TYPE: DNA
235 <213> ORGANISM: Sulfolobus acidocaldarius
237 <400> SEQUENCE: 11
238 tttttccttg tgcttgatga tatcatg 27
240 <210> SEQ ID NO: 12
241 <211> LENGTH: 27
242 <212> TYPE: DNA
243 <213> ORGANISM: Sulfolobus acidocaldarius
245 <400> SEQUENCE: 12
246 tttttccttg tggctgatga tatcatg 27
248 <210> SEQ ID NO: 13

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Input Set : A:\77670-593 Sequence Listing.txt

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249 <211> LENGTH: 33
250 <212> TYPE: DNA
251 <213> ORGANISM: Sulfolobus acidocaldarius
253 <400> SEQUENCE: 13
254 ttttcgctta ttcgatgatga tcttccatcg atg 33
256 <210> SEQ ID NO: 14
257 <211> LENGTH: 27
258 <212> TYPE: DNA
259 <213> ORGANISM: Sulfolobus acidocaldarius
261 <400> SEQUENCE: 14
262 tttacgcttg tgcgatgatga tattatg 27

VERIFICATION SUMMARY

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Input Set : A:\77670-593 Sequence Listing.txt

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